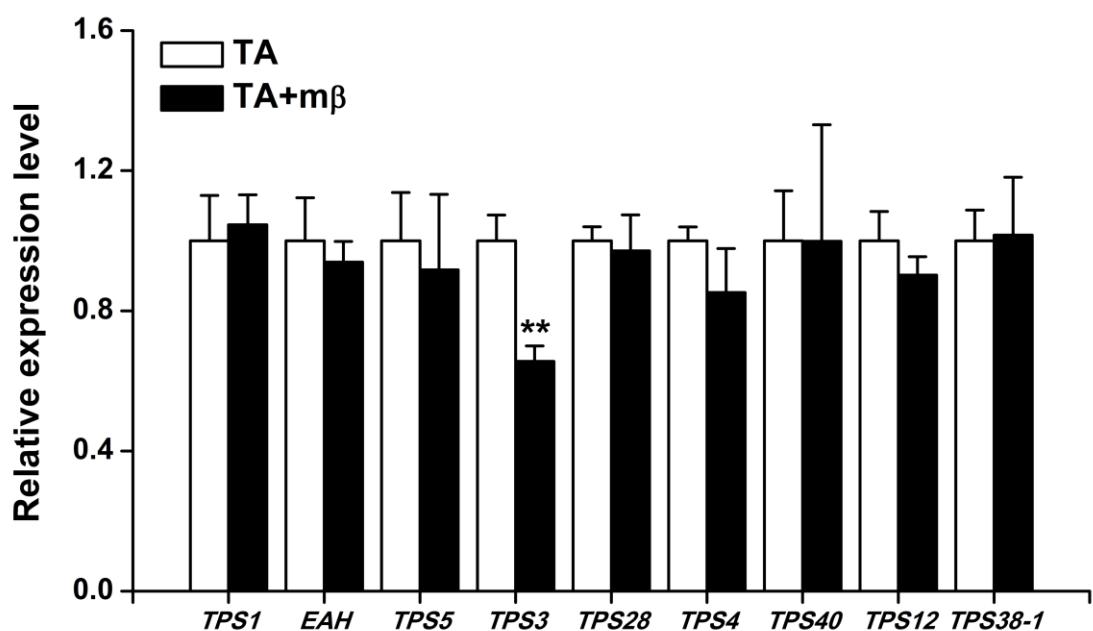


Supplemental Figure 1. Phylogenetic relationships of terpene synthases from plants.

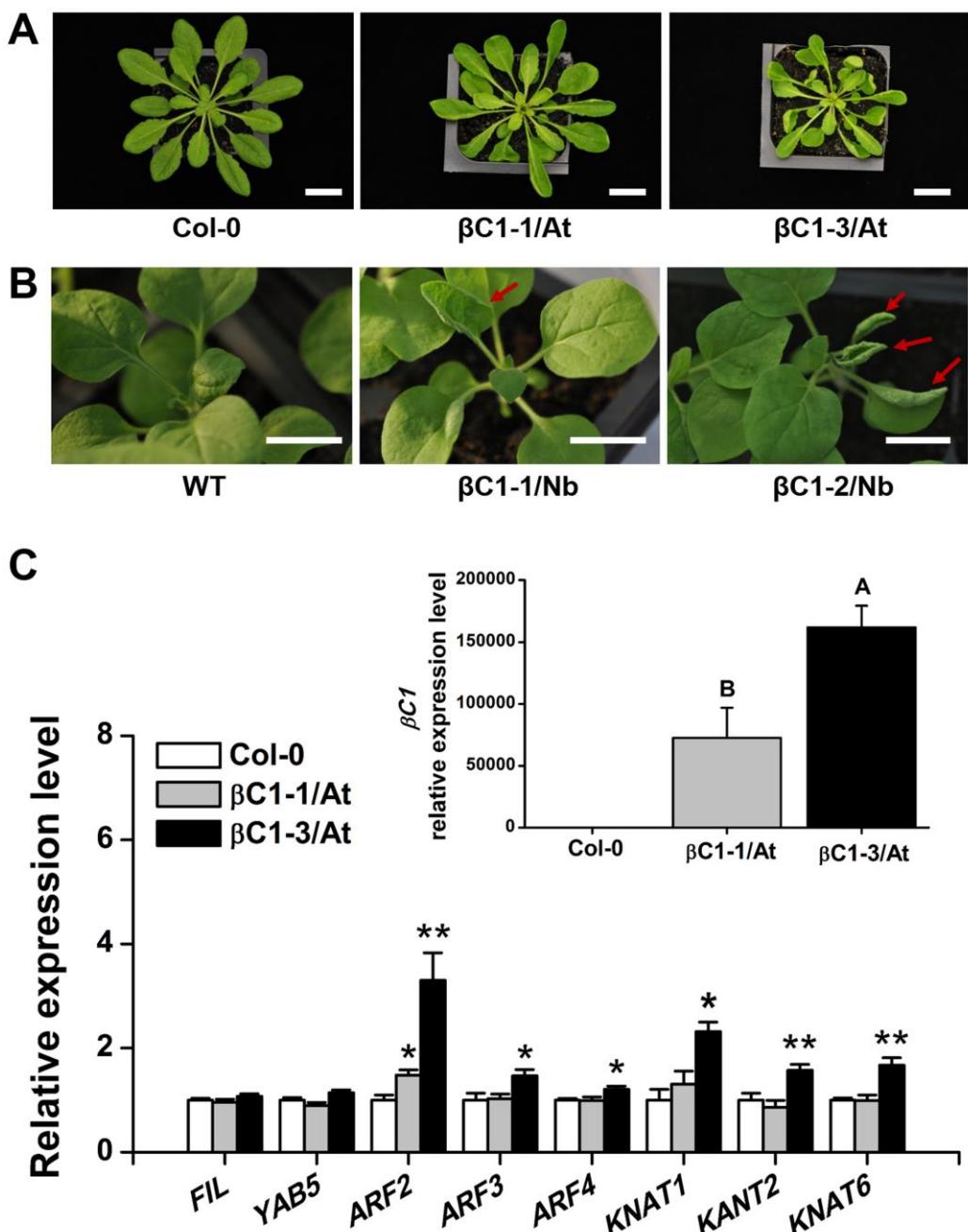
Neighbor-joining phylogenetic trees were constructed using MEGA5.1 based on multiple protein sequence alignments made with ClustalX. Selected protein accession numbers: *Arabidopsis thaliana* (At, TIGR ID): At-TPS10 (AT2G24210), At-TPS03 (AT4G16740), At-TPS21 (AT5G23960); Nt-EAS1: *Nicotiana tabacum* EAS1 (JQ812050); Os-TPS3: *Oryza sativa* TPS3 (DQ872158); Zm-TPS10: *Zea mays* TSP10 (NM_001112380); *Mentha spicata* (Ms, NCBI ID): Ms-LS (L13459). *Solanum lycopersicum* (Sl) TPS were used as

described previously (Falara et al., 2011). *Nicotiana benthamiana* (Nb) TPSs were used as listed Supplemental Dataset 1.



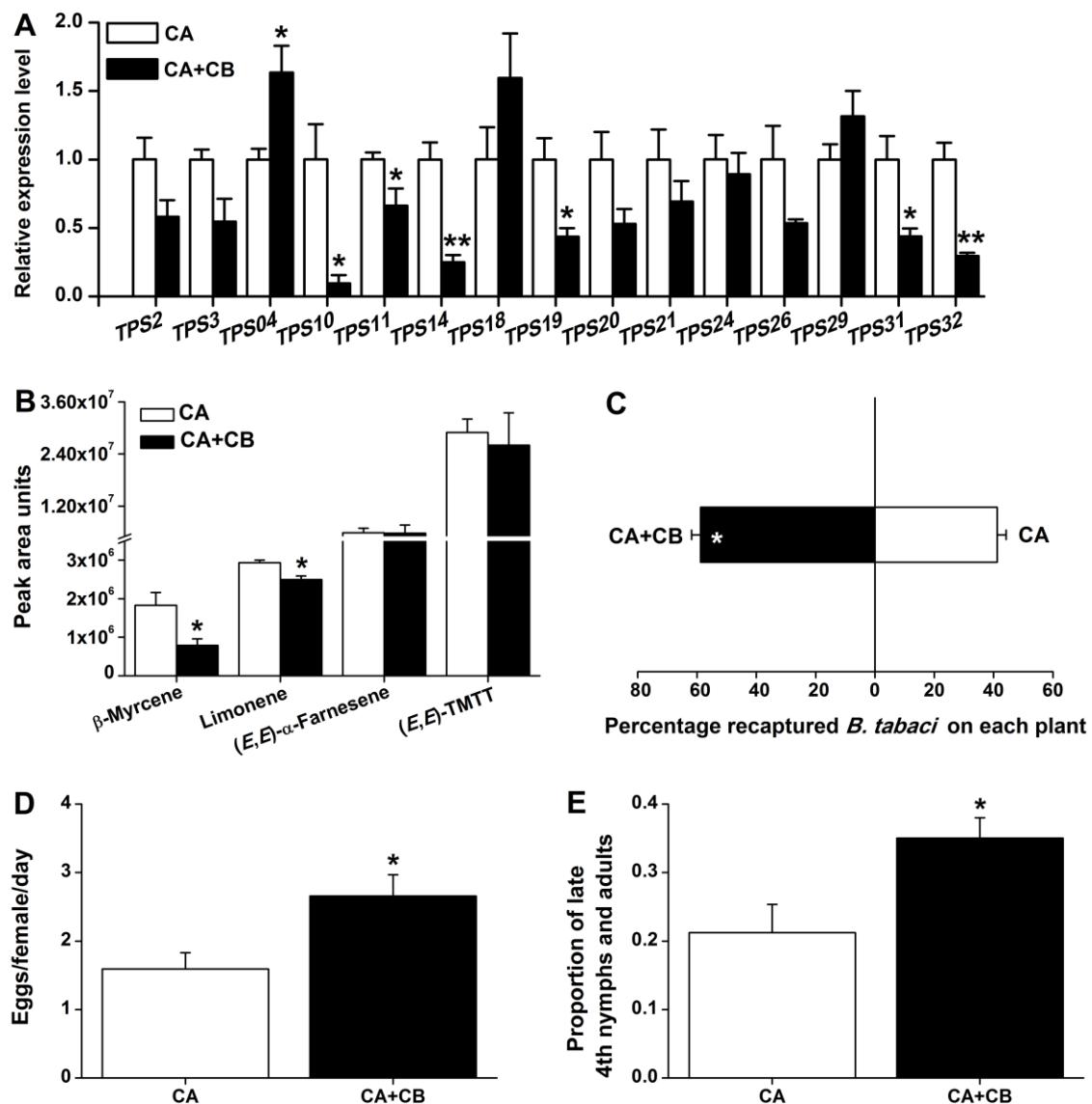
Supplemental Figure 2. Effect of β C1 on terpene synthase transcript levels in *N. benthamiana*.

Relative expression levels of terpene synthase in *N. benthamiana* infected by a mutant Tomato Yellow Leaf Curl China Virus (TYLCCNV). Agroinfiltration of TYLCCNV and a mutant betasatellite encoded a defective β C1 protein (TA+m β) or agroinfiltration of TYLCCNV alone (TA). Values are mean +SE (n=6). Asterisks indicate significant differences in transcript levels between different treatments (**, P< 0.01; Student's t-test).



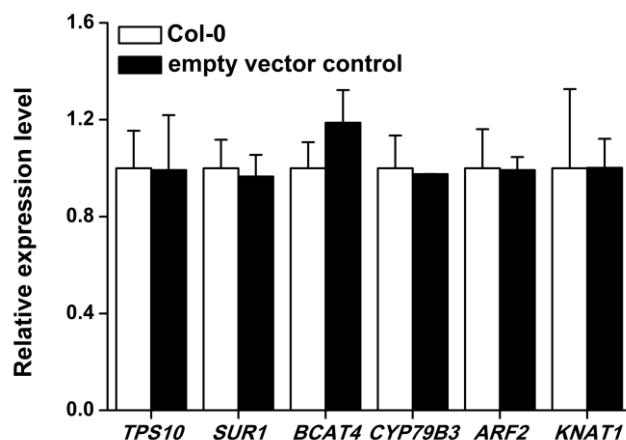
Supplemental Figure 3. Ectopic expression of β C1 affects *Arabidopsis* and *N. benthamiana* leaf development.

Phenotypes of transgenic *Arabidopsis* (A) and *N. benthamiana* (B) lines carrying 35S: β C1 and expression level of leaf developmental regulator genes in transgenic β C1 *Arabidopsis* lines (C). Insert, relative expression levels of β C1 in wild type and two *Arabidopsis* transgenic lines expressing β C1 (β C1-1/At; β C1-3/At). Values are mean +SE (n=5). Bar: 20mm. Letters indicate significant differences among different lines ($P < 0.05$, Duncan's multiple-range test); Asterisks indicate significant differences between different lines (*, $P < 0.05$; **, $P < 0.01$; Student's *t*-test).



Supplemental Figure 4. Bipartite begomovirus increases whitefly attraction and performance on *Arabidopsis* by decreasing terpene synthesis.

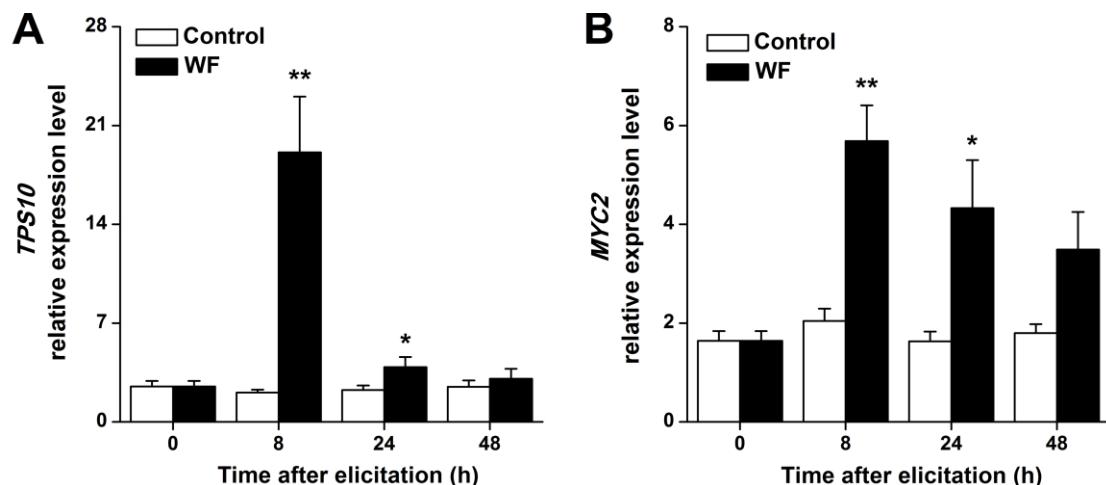
(A) Relative expression levels of terpene synthase in wild type *Arabidopsis* (Col-0) infected by bipartite begomovirus *Cabbage Leaf Curl Virus* (CaLCuV, CA+CB), with single DNA-A infection as a negative control (CA). Values are mean +SE (n=5). (B) Emission of terpenes in CaLCuV-infected *Arabidopsis*. Results were expressed as peak area units per gram of plant fresh weight. (E,E) -TMTT= (E,E) -4,8,12-trimethyltrideca-1,3,7,11-tetraene. Values are mean +SE (n=6). (C) Whitefly preference (as percentage recaptured *B. tabaci* out of 200 released) on CaLCuV-infected *Arabidopsis* (CA+CB) and control *Arabidopsis* (CA). Values are mean +SE (n=8). (D) Daily number of eggs laid per female in CaLCuV-infected *Arabidopsis* (CA+CB) and control DNA-A only infected *Arabidopsis* (CA). Values are mean +SE (n=8). (E) Effect of virus infection on the developmental progression of whitefly (proportion of red eye yellowish 4th instar nymphs and open exuvia in the population) by Day 22. Values are mean +SE (n=8). Asterisks indicate significant differences between different treatments (*, P< 0.05; **, P< 0.01; Student's t-test).



Supplemental Figure 5. Transcript level of different genes in wild type and empty vector transgenic *Arabidopsis*.

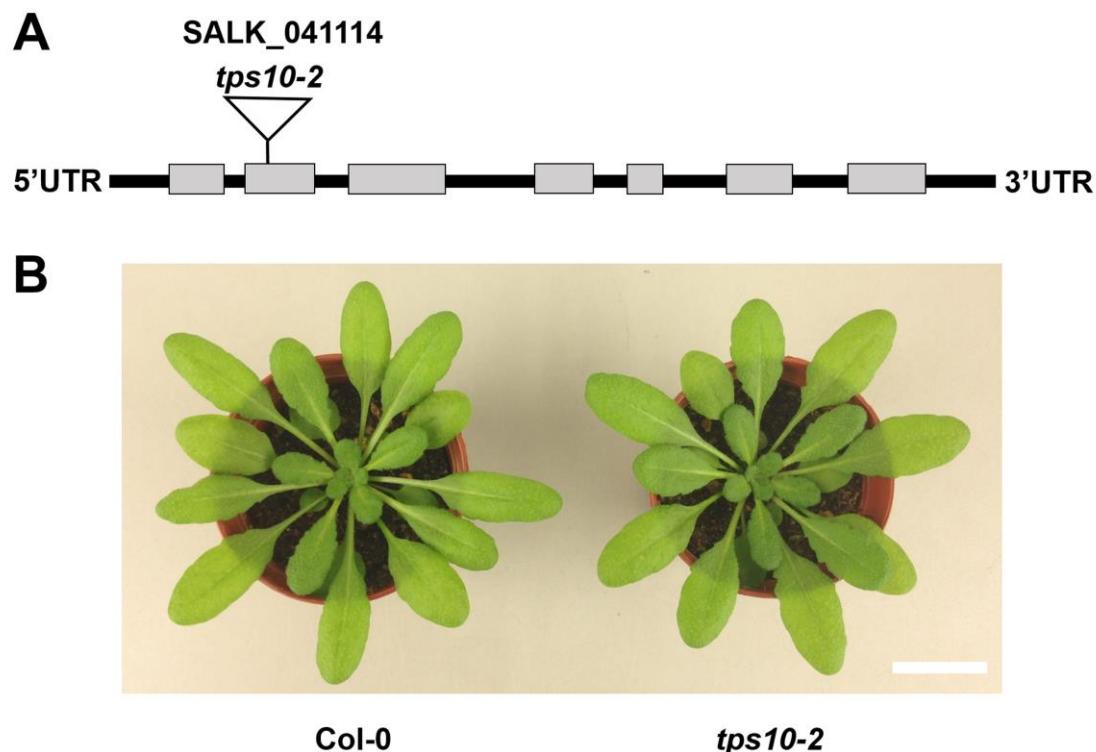
Relative expression levels of *TPS10*, *SUR1*, *BCAT4*, *CYP79B3*, *ARF2*, *KNAT1* in wild type *Arabidopsis* (Col-0) and empty vector transgenic *Arabidopsis*.

Values are mean +SE (n=6).



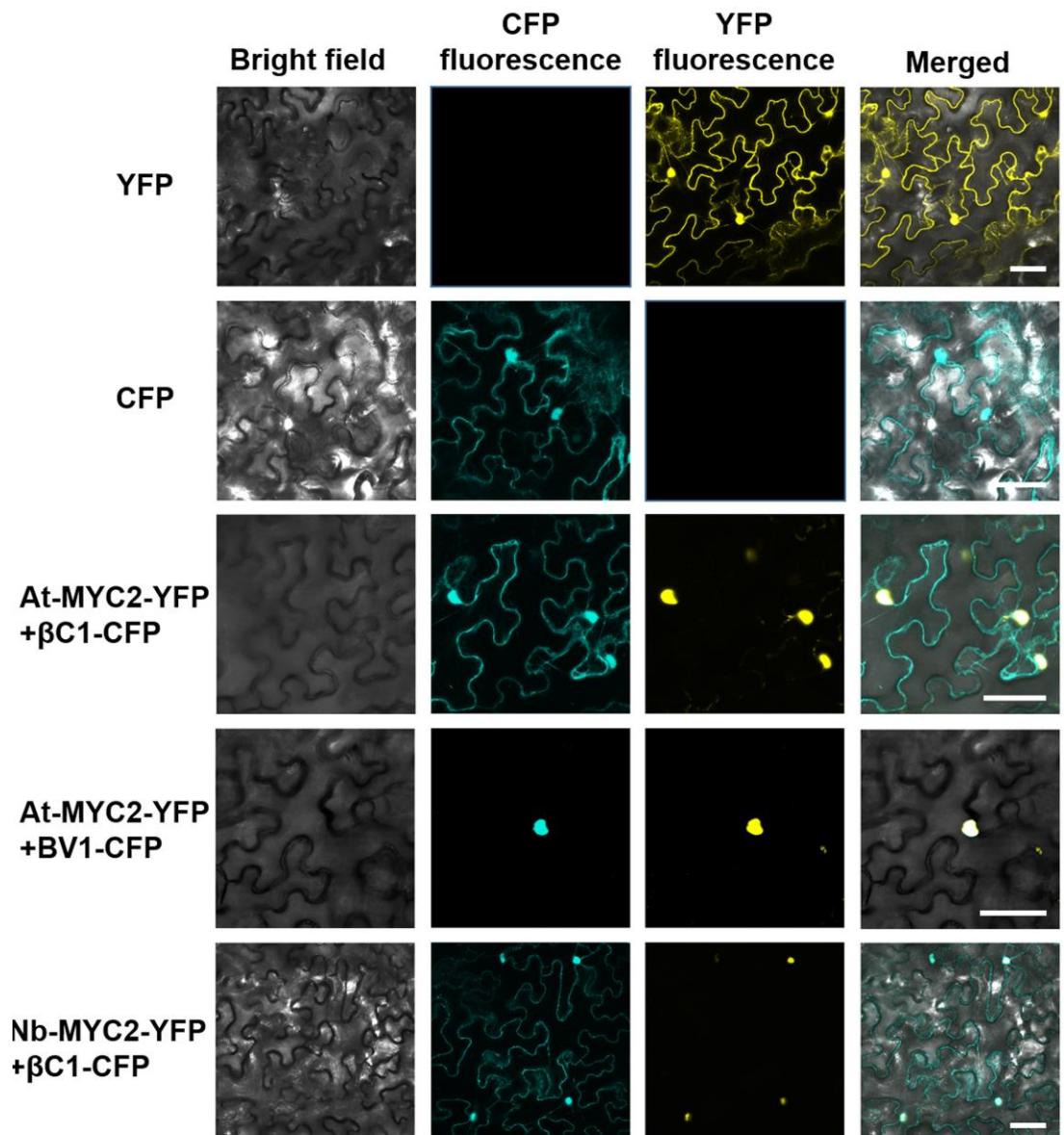
Supplemental Figure 6. Expression profile of At-*TPS10* and At-*MYC2* induced by whitefly feeding.

Relative expression levels of *TPS10* (A) and *MYC2* (B) in *Arabidopsis* plants exposed to whitefly (WF) feeding. Control, untreated plants. Transcript levels were analyzed by RT-qPCR. Values are mean +SE (n=6). Asterisks indicate significant differences in transcript levels between treatment and control (*, P<0.05; **, P<0.01; Student's t-test).



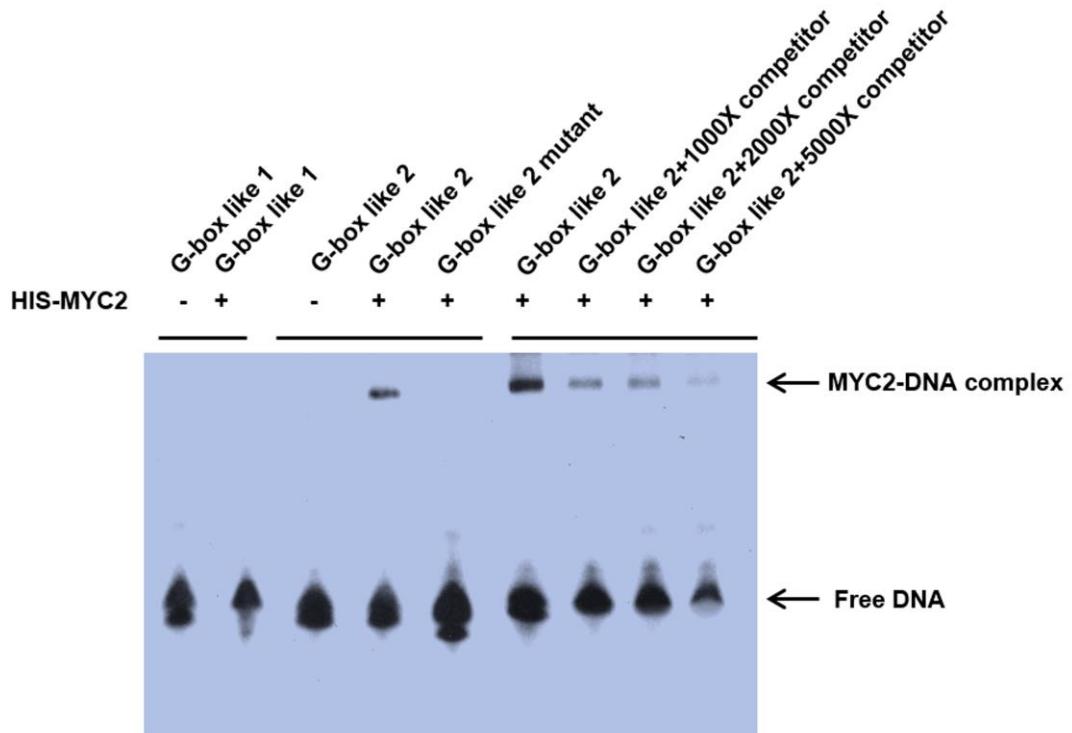
Supplemental Figure 7. Phenotype of *TPS10* T-DNA insertion mutant in *Arabidopsis* (SALK_041114).

(A) Position of T-DNA insertion in the *TPS10* gene. Exons are represented by gray boxes, and untranslated regions (UTR) and introns are represented by black line. (B) Phenotypes of *TPS10* T-DNA insertion mutant (*tps10-2*) compared to wild type *Arabidopsis* (Col-0). Scale bar=20mm.



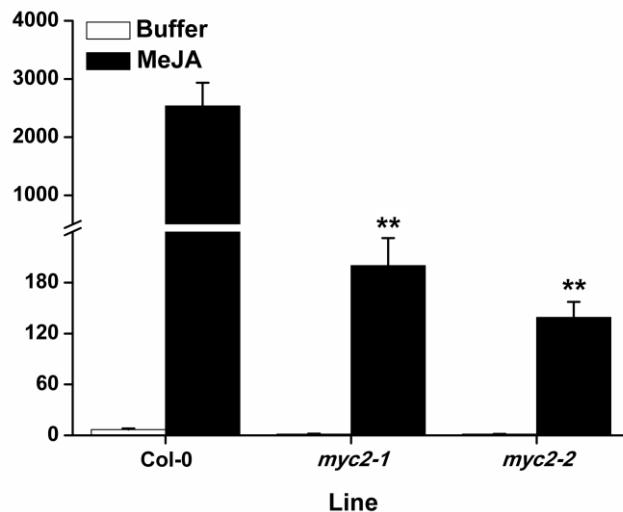
Supplemental Figure 8. Co-localization of TYLCCNB β C1, CaLCuV BV1 protein and plant MYC2 transcription factors.

The indicated constructs containing YFP, CFP, At-MYC2 or Nb-MYC2 fused with YFP and BV1 or β C1 fused with CFP were introduced into tobacco leaf cells by agroinfiltration. After two days, excised leaves were observed under a confocal microscope. Scale bar=50 μ m.



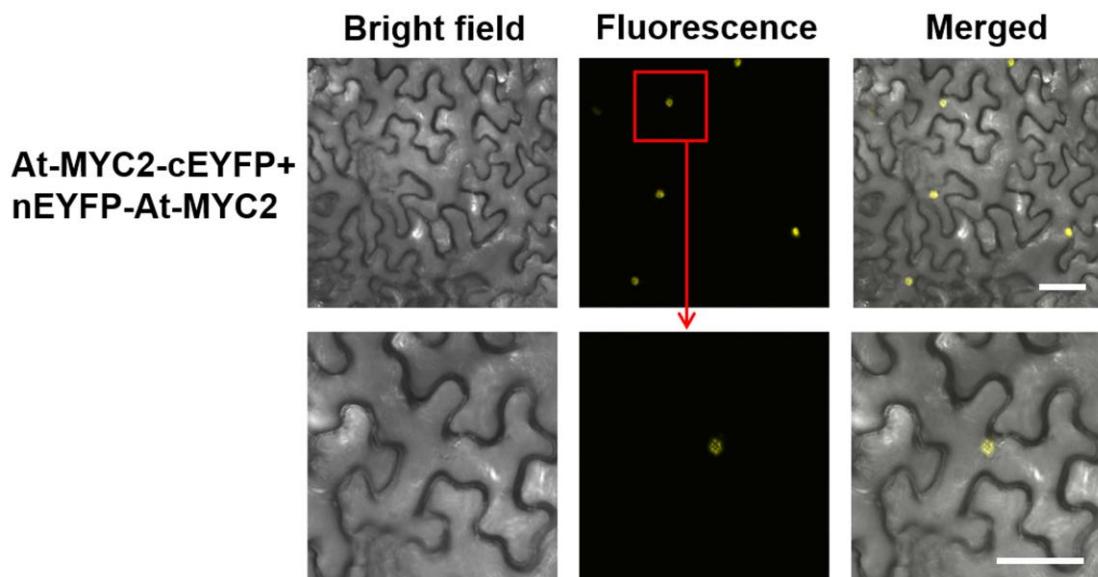
Supplemental Figure 9. EMSA analysis of MYC2 binding to the G-box like Elements.

The recombinant At-MYC2 protein can bind the G-box like 2 element but neither the mutant G-box like 2 probe nor G-box like 1. Competition experiments were performed using unlabelled G-box like 2 element as a competitor in a different fold molar excess.



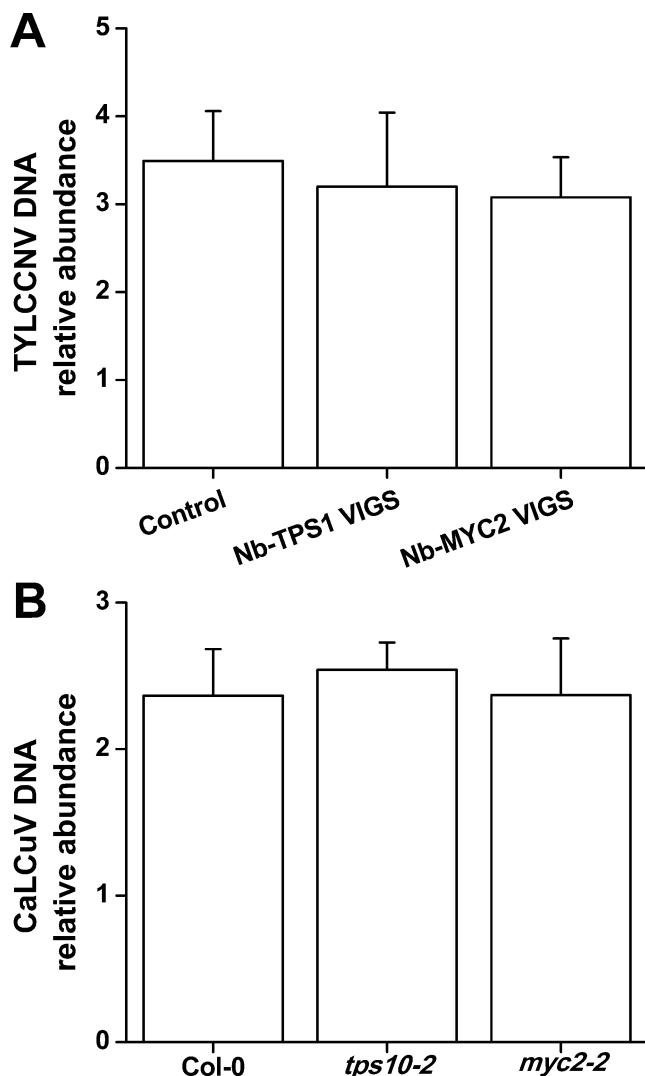
Supplemental Figure 10. Transcript level of *TPS10* in wild type and *myc2* knockout *Arabidopsis*.

Relative expression levels of *TPS10* in wild type *Arabidopsis* (Col-0) and *myc2* after MeJA or mock treatment for 0 h and 6 h. Values are mean +SE (n=6). Asterisks indicate significant differences in transcript levels between WT and mutant. (**, $P< 0.01$; Student's *t*-test).



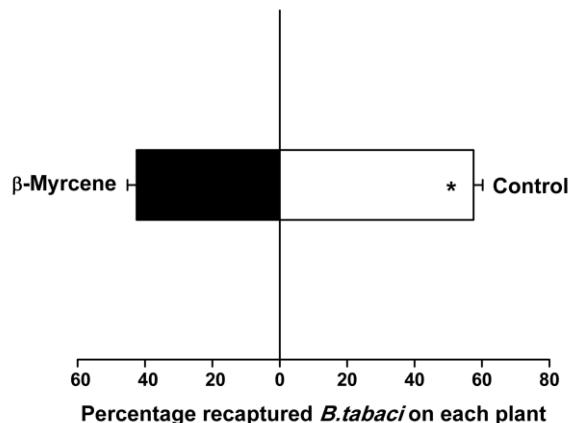
Supplemental Figure 11. Self-interaction of At-MYC2 assayed by BiFC assay.

At-MYC2 was separately fused with the C-terminal or the N-terminal part of EYFP. At-MYC2-cEYFP and nEYFP-At-MYC2 constructs were introduced into tobacco leaf cells by agroinfiltration. After two days excised leaves were observed under a confocal microscope. Scale bar=50 μ m.



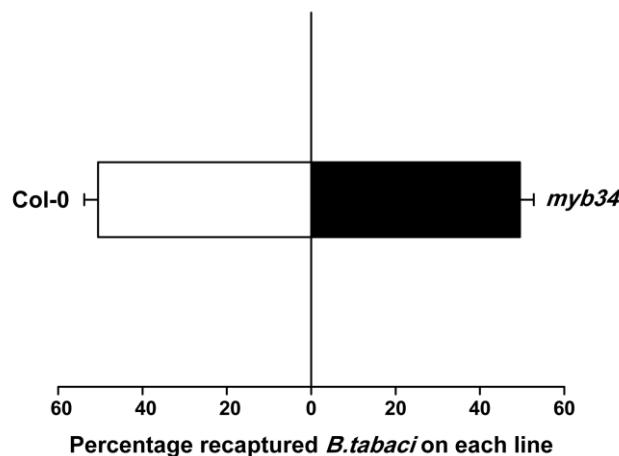
Supplemental Figure 12. The role of MYC2 and TPS in begomoviruses viral titer.

(A) TYLCCNV DNA accumulation was measured by RT-qPCR and normalized to *N. benthamiana* *EF1 α* gene. Values are mean +SE (n=8). (B) CaLCuV DNA accumulation was measured by RT-qPCR and normalized to *Arabidopsis* *Actin2*. Values are mean +SE (n=8).



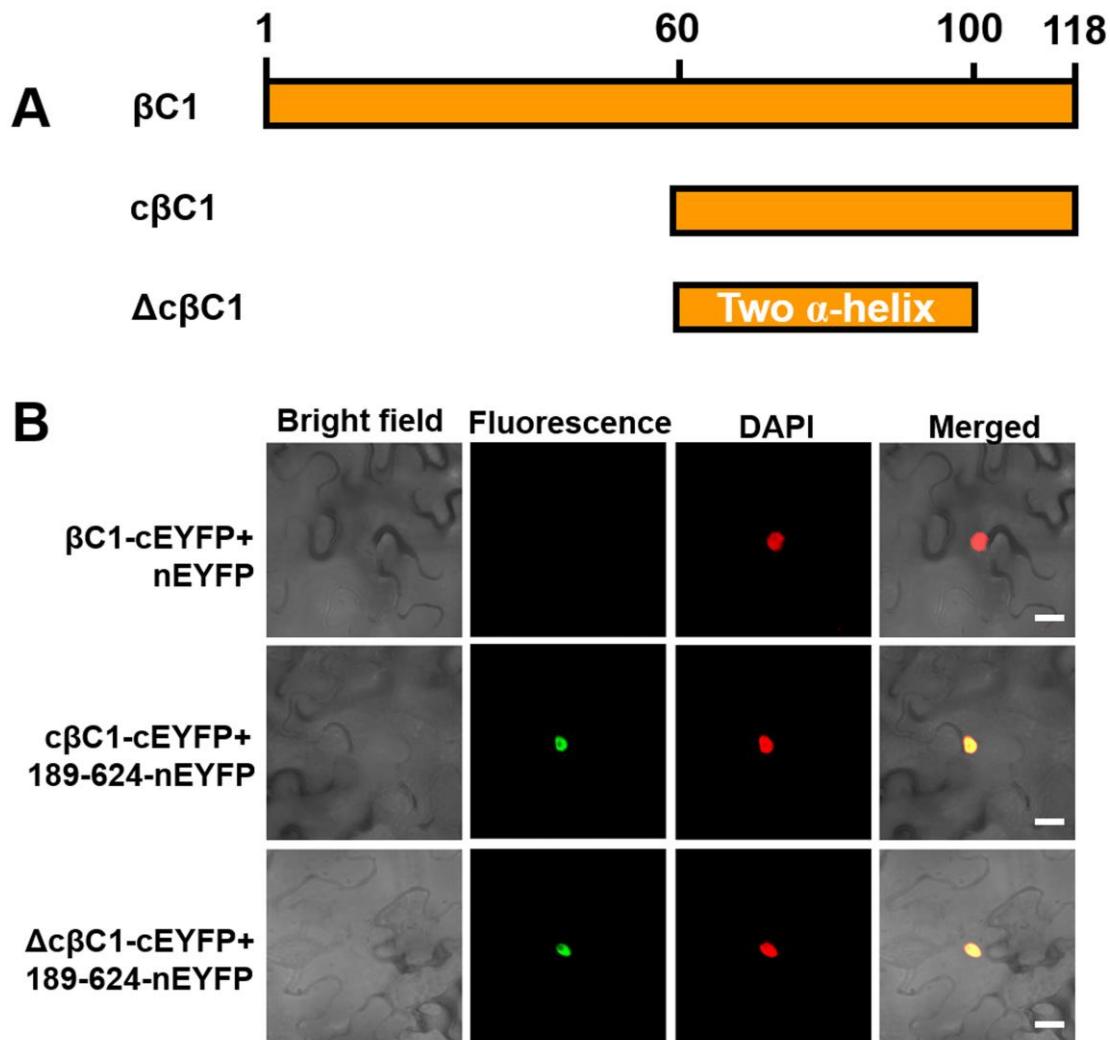
Supplemental Figure 13. The role of β-myrcene in whitefly feeding behavior.

Whitefly preference (as percentage recaptured *B. tabaci* out of 200 released) on β-myrcene treated and non-treated *Arabidopsis* (Control). Bars represent mean +SE (n=8). Asterisks indicate significant differences between treatments (*, P< 0.05; Wilcoxon matched pairs test).



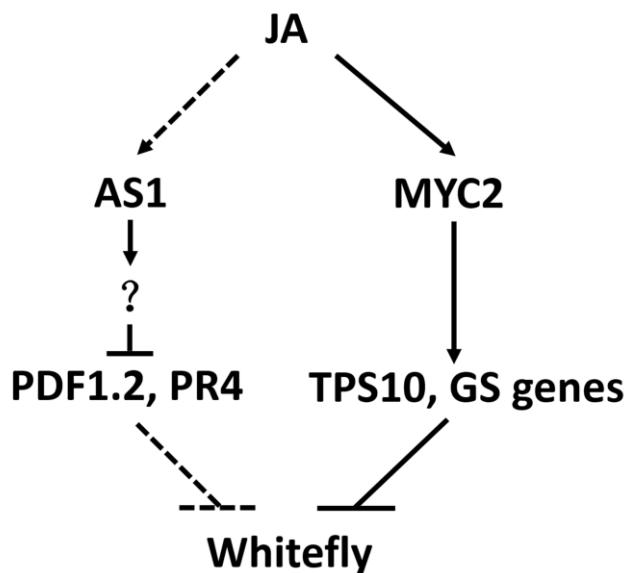
Supplemental Figure 14. The role of glucosinolate biosynthesis related gene *MYB34* in whitefly feeding behavior.

Whitefly preference (as percentage recaptured *B. tabaci* out of 200 released) on *myb34* mutant compared to wild type *Arabidopsis* (Col-0). Bars represent mean +SE (n=8).



Supplemental Figure 15. Helix domain of βC1 is sufficient to bind with MYC2 protein.

(A) Schematic diagrams of two predicted α-helix in the C-terminal of βC1 protein. cβC1, C-terminal of βC1 protein. ΔcβC1, α-helix contained C-terminal deletion of βC1 protein. **(B)** BiFC analysis of βC1 derivative interaction with At-MYC2 N-terminal (189aa-624aa). Either cβC1 or ΔcβC1 was fused with the C-terminal part of EYFP individually. At-MYC2 (189-624) was fused with the N-terminal part of EYFP. *Agrobacterium* strain carrying cβC1- or ΔcβC1-cEYFP along with 189-624-nEYFP constructs were introduced into tobacco leaf cells by agroinfiltration. Two days post inoculation excised leaves were observed under a confocal microscope. Scale bar=50 μm.



Supplemental Figure 16. AS1 and MYC2 regulate different JA pathway against whitefly.

MYC2 is induced by JA and positively regulates plant resistance to whitefly by directly activating *TPS10* and glucosinolate synthase (GS) genes. AS1 negatively regulates *PDF1.2* and *PR4*. However, whether and how AS1 is responsive to JA and whether *PDF1.2* and *PR4* are involved in whitefly resistance by direct transcriptional regulation of AS1 or via an unknown factor is unclear.

Supplemental Table**Supplemental Table 1. DNA primers used in this study.**

Gene	Sequence (5'-3')	Purpose
Nb-EAH-F	ATGCAATTCTTCAGCTTGGTTCC	RT-qPCR
Nb-EAH-R	GACATGGTGCAGTTCTCCACAA	RT-qPCR
Nb-TPS1-F	TTAAAACGAACAAAAACAATACCCCTCAT	RT-qPCR
Nb-TPS1-R	CTCTTGAGCATACTTTGTGCAACC	RT-qPCR
Nb-TPS5-F	ACATTGTTCAAGCAACACATCAAGAA	RT-qPCR
Nb-TPS5-R	CATCAAGAGTTGTAACAAGAGCATT	RT-qPCR
Nb-TPS3-F	TCACCAACCCAATTACGAAAGAGA	RT-qPCR
Nb-TPS3-R	CGTTTATCATTTCATGTCTCCT	RT-qPCR
Nb-TPS28-F	TGCTTCATTATTGGGCATGA	RT-qPCR
Nb-TPS28-R	CCCGTCACAAGTTGTCCTT	RT-qPCR
Nb-TPS4-F	CGGATGAATTGAAGAGGGGTGATGTT	RT-qPCR
Nb-TPS4-R	ATGTGCTGTTCTGCAATATTCTTT	RT-qPCR
Nb-TPS12-F	CGGCAGTGAACCTGATGAGA	RT-qPCR
Nb-TPS12-R	CAACTCCAACATGTGCTGCT	RT-qPCR
Nb-TPS38-1-F	ACGCAATAGAGCGACTACCTGACTA	RT-qPCR
Nb-TPS38-1-R	TGTTTGTATCCATGCATTCTCA	RT-qPCR
Nb-TPS40-F	TAATGCACAAAGTGCCCACAACGTT	RT-qPCR
Nb-TPS40-R	AACAGATTCCCTCATTGTCCAATA	RT-qPCR
Nb-MYC2-F	GAAAAGAGGCCAAAGAACCGAGGAA	RT-qPCR
Nb-MYC2-R	CTTCAGCTCATTAATTATATGAAATT	RT-qPCR
Nb-EF1α-F	TGGTGTCCCTAAGCCTGGTATGGTTG	RT-qPCR
Nb-EF1α-R	ACGCTTGAGATCCTTAACCGCAACATTCTT	RT-qPCR
At-Tubulin2-F	TCAAGAGGTTCTCAGCAGTA	RT-qPCR
At-Tubulin2-R	TCACCTTCTTCATCCGCAGTT	RT-qPCR
At-TPS21-F	TCGCCTTGGTGTCTCCTATCAC	RT-qPCR
At-TPS21-R	CTTGAACCTCCCATTTCGTCC	RT-qPCR
At-TPS11-F	CACTTGGACAACGACAGA	RT-qPCR
At-TPS11-R	CTTGGAAAGTAATGAAGCTGCAAG	RT-qPCR
At-TPS2-F	CAACGATACTGCTCACCTTT	RT-qPCR
At-TPS2-R	TGTCTACGTGCCTTCCCTCAC	RT-qPCR
At-TPS3-F	GAATTAGCGAGAGGCGACAC	RT-qPCR
At-TPS3-R	CTGATAAACGCACTGAGCCA	RT-qPCR
At-TPS04-F	TCACCTTCAGCAACTGCATC	RT-qPCR
At-TPS04-R	TTTTCTTCGTAGCGGCTGT	RT-qPCR
At-TPS10-F	GTACATGCAAAATGCTCGGAT	RT-qPCR
At-TPS10-R	TTGGTGTGGACAAAGTCTC	RT-qPCR
At-TPS11-F	CACTTGGACAACGACAGA	RT-qPCR
At-TPS11-R	CTTGGAAAGTAATGAAGCTGCAAG	RT-qPCR
At-TPS14-F	AGGCGAAGAACTAACAAAAGAG	RT-qPCR

At-TPS14-R	AGAATGGACATGGATTCAAGACA	RT-qPCR
At-TPS18-F	ACCGAAAGGACGATCATACG	RT-qPCR
At-TPS18-R	GCTGTCACCAACCCAACTTT	RT-qPCR
At-TPS19-F	GCTGGTGAAGACATGCTCA	RT-qPCR
At-TPS19-R	AACCTCCCCTCTCCACCTCT	RT-qPCR
At-TPS20-F	TGGAATAGTGACTGGGGAG	RT-qPCR
At-TPS20-R	TTCCCTGTGGCAATCTCTCCT	RT-qPCR
At-TPS21-F	TCGCCTTGGTGTCTCCTATCAC	RT-qPCR
At-TPS21-R	CTTGAACCTCCCATTTCGTCC	RT-qPCR
At-TPS40-F	TCCACTTTACTGTGCTTCTC	RT-qPCR
At-TPS40-R	CTTGCTTCATAGTTCATCTCGT	RT-qPCR
At-TPS26-F	GATTCAAAGGGAGCAATGGA	RT-qPCR
At-TPS26-R	TGTGCACTGAGAGATGAGGC	RT-qPCR
At-TPS29-F	AACCCGAAAACAACAAGAC	RT-qPCR
At-TPS29-R	CAAATGGATGAGGCGAACATCT	RT-qPCR
At-TPS31-F	GGCGGTGACGTTAACATCT	RT-qPCR
At-TPS31-R	ATTGATGATTCCGCGAGAC	RT-qPCR
At-TPS32-F	CCTTCAGAAATTGAGGCTG	RT-qPCR
At-TPS32-R	ACAAGTGGCCAAGTCCAAC	RT-qPCR
At-MYC2-F	CAAGGAGGAGTGTGTTGGGATGC	RT-qPCR
At-MYC2-R	GTCGAAAAATTAGTTCTCGGGAG	RT-qPCR
KNAT1-F	TGTTGTTCCACATATGAGCTCT	RT-qPCR
KNAT1-R	TCATGATCAGATCGGAAGCAAT	RT-qPCR
KNAT2-F	TTCCGCTCGACGGAAGAC	RT-qPCR
KNAT2-R	AATCGGACGGCATCATCAC	RT-qPCR
KNAT6-F	GATGTCACGGAGAGTCTCATG	RT-qPCR
KNAT6-R	CGGCGGAGGAACATAGCA	RT-qPCR
ARF2-F	CCCATTGGTCGCCTCATACC	RT-qPCR
ARF2-R	GATATCAACAAGAAATCTCC	RT-qPCR
ARF3-F	CGCCTACTCAATAACCGATCATC	RT-qPCR
ARF3-R	ACGGCCCACACCAAATGTT	RT-qPCR
ARF4-F	CGCTTAAATCATTCCCGCAAT	RT-qPCR
ARF4-R	ACTTGTTGGCTTGGTAAGCAAAG	RT-qPCR
FIL-F	AAACCAACATGCCCAACAG	RT-qPCR
FIL-R	TCACACCAACGTTAGCAGCTG	RT-qPCR
YAB5-F	ACGCCCTAATTCCAGGCAAC	RT-qPCR
YAB5-R	GTTGCTCAGTTATGGTACGAG	RT-qPCR
BCAT4-F	CTGTAUTGGCACTGCTTCCA	RT-qPCR
BCAT4-R	ATAGCTTCCGAGCCAATGTT	RT-qPCR
CYP79B3-F	CTTGCTTACCGCTGATGAA	RT-qPCR
CYP79B3-R	GCGTTTGATGGTTGTCTG	RT-qPCR
GSTF11-F	CGCTGTGGCTCTACCCCTAG	RT-qPCR
GSTF11-R	TCCAGGACCTTGTGAACTT	RT-qPCR

SUR1-F	TGCAAAGAAGAACAAAGATACTCAAA	RT-qPCR
SUR1-R	TCTTGGGACAGACGACACAG	RT-qPCR
UGT74B1-F	ATCCTGAGCATGGCAGAGTT	RT-qPCR
UGT74B1-R	CCCTTCAAAGCCATTAAACGA	RT-qPCR
MYB34-F	AAGAACGGTTGAAGCAAA	RT-qPCR
MYB34-R	CTAGCGGAACCGGATGAATA	RT-qPCR
MYB51-F	AGCTCGTGACTACCAGGAA	RT-qPCR
MYB51-R	GGAGGTTATGCCCTGTGTG	RT-qPCR
β C1-F	ATCCCACCATTCGACTTCAA	RT-qPCR
β C1-R	TTCTACTGGGCTTCTCCA	RT-qPCR
CalCuV-F	TGAATCACCTCAACTATGATACT	RT-qPCR
CalCuV-R	CAATTATAAGGGCTGGAGATCCAA	RT-qPCR
TYLCCNV-F	AGAAACGCAAGGTCTGAGGA	RT-qPCR
TYLCCNV-R	TATCTGGACGGCCAAAATC	RT-qPCR
pGEX-At-MYC2-F	CCCGGGTATGACTGATTACCGGCTACAA	protein expression
pGEX-At-MYC2-R	GCGGCCGCTTAACCGATTTGAAATCA	protein expression
pMAL-At-MYC2-F	GGCAGGAAGGATTCAATGACTGATTACCGGCTAC	protein expression
pMAL-At-MYC2-R	GGCCGCTGCAGTTAACCGATTTGAAATC	protein expression
PET28b-At-MYC2-F	GCACTCATATGATGACTGATTACCGGCTAC	protein expression
PET28b-At-MYC2-R	GCACAGGGCCGACCGATTTGAAATCAA	protein expression
pMAL-Nb-MYC2-F	GGATCCATGACTGATTACAGATTACCCAC	protein expression
pMAL-Nb-MYC2-R	GTCGACTTAGCGTGTTCAGCAACTCTGG	protein expression
pGEX- β C1-F	GCGCGGGATCC ATGACTATCAAATACAAC	protein expression
pGEX- β C1-R	CGGCCGAATTCTCATACATCTGAATTGT	protein expression
pGEX-BV1-F	CAGCGGATCCTATCCTACAAAGTTAGCGTGGG	protein expression
pGEX-BV1-R	ATCCCTCGAGTCATTAACCTAAATAATCAAGATCGTAAG	protein expression
AD-At-MYC2-F	GGCAGCATATGATGACTGATTACCGGCTAC	Yeast two-hybrid
AD-At-MYC2-R	GACTGCCGGGTTAACCGATTTGAAATC	Yeast two-hybrid
BD- β C1-F	GGCCGAATTCTCATGACTATCAAATACAAC	Yeast two-hybrid
BD- β C1-R	CGCGGGATCCTCATACATCTGAATTGT	Yeast two-hybrid
1391-PTPS10-F	GCGGCCTGCAGCGAACACATTCTATAATT	Promoter

		construct
1391-PTPS10-R	TCGACGTCGACTACGTAACCTTCAGGTGA	Promoter construct
n- At-MYC2-F	AGTGCAGTACCATGACTGATTACCGGCTAC	BiFC
n- At-MYC2-R	AGTGTCCCGGGCCACCGATTTGAAATCA	BiFC
n-1-624-F	AGTGCAGTACCATGACTGATTACCGGCTAC	BiFC
n-1-624-R	AGTGTCCCGGGCCACCGATTTGAAATCAA	BiFC
n-1-188-R	ATTGTCCCGGGCCTGCAAACGCTTACCAGC	BiFC
n-189-624-F	ATTGTGGTACCGGGTAACCGGGTTGGGT	BiFC
n-189-445-R	ATTGTCCCGGGCGTTGCTGGCTTCTCCT	BiFC
n-446-624-F	AGTGCAGTACCGGTAGAGAAGAGCCACTAAA	BiFC
n-189-501-R	AGTGTCCCGGGCCTACTTGATTAAGCTCG	BiFC
n-501-624-F	AGTGCAGTACCGAGCTAAATCAAAGTA	BiFC
n-431-624-F	AGTCGGTACCGCAGTAGAGAAACGTC	BiFC
n-Nb-MYC2-F	GCCCCGCTCGAGCTATGACTGATTACAGATT	BiFC
n-Nb-MYC2-R	ACTAAGGATCCCGTGTTCAGCAACTCT	BiFC
βC1-C-F	CGGCCGAATTCTGACTATCAAATACAAC	BiFC
βC1-C-R	GCGCGGGATCCCTACATCTGAATTGTAA	BiFC
cβC1-C-F	CGCGCGAATTCTGAAACATTTAGAAGAAGG	BiFC
ΔcβC1-C-R	TCAAGGGATCCCTCTACTGGGGCTTCTT	BiFC
At-MYC2-YFP-F	AGTCTCCTAGGAATGACTGATTACCGGCT	localization
At-MYC2-YFP-R	AGTCGGCCGGAACCGATTTGAAATCAA	localization
βC1-CFP-F	GCGCGCTCGAGATGACTATCAAATACAAC	localization
βC1-CFP-R	GCGCGGGATCCCTACATCTGAATTGTAA	localization
Nb-MYC2-YFP-F	GCCCCGCTCGAGCTATGACTGATTACAGATT	localization
Nb-MYC2-YFP-R	ACTAAGGATCCCGTGTTCAGCAACTCT	localization
Nb-TPS1-F	ATAATTCTAGAGGCAACATGGTTCAACATCTCCT	VIGS
Nb-TPS1-R	GTATGGATCCAAAATAACTCCTAATGCCAAAA	VIGS
Nb-MYC2-F	GTGCACATCTAGATCTAACTCCTTGAGGG	VIGS
Nb-MYC2-R	ATAAGGATCCCACGTCGAAGCAGAGAGGCAA	VIGS
Region I-F	GTAGAGGTTTAGTCTCGTG	ChIP-RT-qPCR
Region I-R	AAGAGTCGAGCTGGTCGG	ChIP-RT-qPCR
Region II-F	GCACAGTTAGGCCAACCT	ChIP-RT-qPCR
Region II-R	AAGGTAGATTACTCCATGG	ChIP-RT-qPCR
Region III-F	GCCATCTATCCACCTAGTT	ChIP-RT-qPCR
Region III-R	GATAACCTCCTCTCCTAG	ChIP-RT-qPCR
Region IV-F	TGTGTGGATAGTAACCTTT	ChIP-RT-qPCR
Region IV-R	GCAGGAGAGTGGCCATATTG	ChIP-RT-qPCR
Actin2-F	CGTTTCGCTTCCTAGTGTAGCT	ChIP-RT-qPCR
Actin2-R	AGCGAACGGATCTAGAGACTCACCTG	ChIP-RT-qPCR

Supplemental methods

Constructs

About 1.8 kb DNA sequences upstream of the *AtTPS10* transcription start site were amplified with *Pfu* DNA polymerase (Thermo Scientific) using primers listed in Supplemental Table 1 and the amplified DNA fragment was ligated into the binary vector pCAMBIA 1391b. G-box like 2 mutated *At-TPS10* promoter fragments were chemically synthesized by Genescrypt, USA.

Full-length open reading frames encoding At-MYC2, Nb-MYC2, *BV1* and *βC1* without a stop codon were amplified by PCR using *Pfu* DNA polymerase (Thermo Scientific) with primers listed in Supplemental Table 1. The DNA fragments were cloned into pBA-YFP, pBA-CFP, and pGreen-pSAT1 serial vectors to generate fusion genes with YFP, CFP, cEYFP or nEYFP at the amino- or carboxy terminus (Liu et al., 2009). Different derivatives of MYC2 and *βC1* were cloned into pGreen-pSAT1-nEYFP-C1 and assayed along with pGreen-pSAT1-*βC1*-cEYFP.

DNA fragments encoding full-length At-MYC2, Nb-MYC2, *BV1* and *βC1* were cloned into pGEX-4T or pMAL-c2 to generate GST or MBP fusion constructs and transformed into *Escherichia coli* BL21 (DE3).

For VIGS experiments, partial coding sequences of Nb-*TPS1* and Nb-MYC2 were amplified using *Pfu* DNA polymerase (Thermo Scientific) with primers listed in Supplemental Table 1. The DNA fragments were cloned into *psTRV2* (Qu et al., 2012). Plasmids were introduced into *Agrobacterium tumefaciens* AGL or C58C1 strain by electroporation. 35S:MYC2-GFP was transformed into *myc2-2* mutant to generate GFP-tagged MYC2 complementation line 35S:MYC2-GFP/*myc2-2*. *Arabidopsis* transformations were performed using the floral-dip method (Clough and Bent, 1998; Zhang et al., 2006).

Electrophoretic Mobility Shift Assay (EMSA)

Full-length open reading frames encoding At-MYC2 was introduced into pET28b to generate 6XHIS fusion constructs and transformed into *Escherichia coli* BL21 (DE3). His-MYC2 was purified using His-Trap (GE healthcare)

according to the manufacturer's instructions. The fragment containing G-box like 1 (CACAAATATTGTGCTACAAGTGACTTAACGTACTC), G-box like 2 (GTTTGAGATGTCAAGCACATGTTTATTCGTTG) and a mutant G-box like 2 (GTTTGAGATGTCAAGTTCAAATTTATTCGTTG) were labeled by Biotin. EMSA was performed using a LightShift Chemiluminescent EMSA Kit (Thermo) according to the manufacturer's instructions.

Supplemental references

- Clough, S.J., and Bent, A.F.** (1998). Floral dip: a simplified method for *Agrobacterium*-mediated transformation of *Arabidopsis thaliana*. *Plant J.* **16**, 735-743.
- Zhang, X., Henriques, R., Lin, S.S., Niu, Q.W., and Chua, N.H.** (2006). *Agrobacterium*-mediated transformation of *Arabidopsis thaliana* using the floral dip method. *Nat. Protoc.* **1**, 641-646.